January 1999
Volume 89, Number 1
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Letter to the Editor
A Model for the Temporal Buildup of *Polymyxa betae.* C. R. Webb, C. A. Gilligan, and M. J. C. Asher. First and second authors: Department of Plant Sciences, University of Cambridge, Downing Street, Cambridge, CB2 3EA, United Kingdom; and first and third authors: IACR-Broom's Barn, Higham, Bury St. Edmunds, Suffolk, IP28 6NP, United Kingdom. Phytopathology 89:30-38. Accepted for publication 16 September 1998. Copyright 1999 The American Phytopathological Society.

Biological Control
Effect of Nectar on Microbial Antagonists Evaluated for Use in Control of Fire Blight of Pome Fruits. P. L. Pusey. United States Department of Agriculture, Agricultural Research Service, Tree Fruit Research Laboratory, 1104 N. Western Avenue, Wenatchee, WA 98801. Phytopathology 89:39-46. Accepted for publication 28 August 1998. This article is in the public domain and not copyrightable. It may be freely reprinted with customary crediting of the source. The American Phytopathological Society, 1999.

Under warm, dry conditions, *Erwinia amylovora* can become established in relatively high populations on apple (*Malus domestica*) or pear (*Pyrus communis*) flower stigmas, and subsequent wet conditions facilitate its movement to the flower hypanthium where infection generally is initiated through the nectarthodes. Research on biological control of fire blight has focused mainly on the flower stigma, and knowledge is lacking regarding the effect of nectar on microbial antagonists in the flower hypanthium. The biocontrol agents *Pseudomonas fluorescens* strain A506 and *Pantoea agglomerans* strain C9-1 were cultured in a basal liquid medium with various concentrations (0 to 50% total sugar) of sucrose or synthetic nectar (sucrose/glucose/fructose, 2:1:1). Strain A506 showed less growth and lower survival than strain C9-1 at high sugar levels, and A506 was less effective than C9-1 as a preemptive antagonist of *E. amylovora* in high-sugar media. Both antagonist strains were less tolerant to high sugar levels than *E. amylovora* (strain Ea153). The same bacteria were cultured in a medium with 25% total sugar consisting of various proportions of sucrose, glucose, and fructose, and growth response correlated strongly with solute potential. When 28 microbial strains were cultured in synthetic nectar (25% total sugar) and ranked based on growth, strains clustered according to taxonomic group. Yeasts were most osmotolerant, followed by strains of *E. amylovora, Pantoea agglomerans, Bacillus* spp., and *Pseudomonas* spp. Further studies done in planta are necessary to determine whether osmotolerance of antagonists is advantageous in the biological control of fire blight.

Ecology and Population Biology
Suppression of *Fusarium solani* **f. sp.** *phaseoli* **on Bean by Aluminum in Acid Soils.** Hiromitsu Furuya, Tadashi Takahashi, and Tsutomu Matsumoto. Department of Agriculture, Akita Prefectural College of Agriculture, Ogata, Akita, 010-0444, Japan. Phytopathology 89:47-52. Accepted for publication 28 September 1998. Copyright 1999 The American Phytopathological Society.

The severity of bean root rot caused by *Fusarium solani* f. sp. *phaseoli* in vitro was studied with regard to exchangeable soil aluminum for 25 soil samples collected from northeastern Honshyu island, Japan. Of these, 24 were Andosols, typically acidic and of volcanic ash origin. Disease severity was assessed based on the number of lesions produced by the pathogen on a 6-cm section of bean stem buried and incubated for 8 days at 25°C in artificially infested soil samples. The number of lesions differed considerably among soil samples. In all soils in which disease incidence was very low, macroconidial germination was strongly inhibited. The inhibition was observed in all soil samples with exchangeable aluminum contents of at least 0.4 meq/100 g of soil, although it is unclear if this concentration is the lowest limit for inhibition. When soil pH was 5.6 or lower, higher amounts of exchangeable aluminum were detected from soils in which the major clay mineralogy was chloritized 2:1 minerals, while no or limited amounts of aluminum were detected from soils in which the major clay mineralogy was allophane/imogolite. Macroconidial germination and disease incidence are thus closely related to clay mineralogy, which regulates the behavior of exchangeable aluminum. *Additional keywords*: allophanic Andosols, residual soil fungistasis.

Etiology
Causal Role of *Xylella fastidiosa* **in Oleander Leaf Scorch Disease.** A. H. Purcell, S. R. Saunders, M. Hendson, M. E. Grebus, and M. J. Henry. First, second, and third

authors: Department of Environmental Science, Policy and Management, University of California, Berkeley 94720-3112; fourth author: Department of Plant Pathology, University of California, Riverside 92521; fifth author: University of California Cooperative Extension, 21150 Box Springs Rd., Moreno Valley 92557.

A lethal leaf scorch disease of oleander (*Nerium oleander*) appeared in southern California in 1993. A bacterium, *Xylella fastidiosa*, was detected by culturing, enzyme-linked immunoassay, and polymerase chain reaction in most symptomatic plants but not in symptomless plants or negative controls. Inoculating oleanders mechanically with *X. fastidiosa* cultures from diseased oleanders caused oleander leaf scorch (OLS) disease. The bacterium was reisolated from inoculated plants that became diseased. Three species of xylem sap-feeding leafhoppers transmitted the bacterium from oleander to oleander. The bacterium multiplied, moved systemically, and caused wilting in Madagascar periwinkle (*Catharanthus rosea*) and leaf scorch in periwinkle (*Vinca major*) in a greenhouse after inoculation with needle puncture. No bacterium was reisolated from grapevine (*Vitis vinifera*), peach (*Prunus persica*), olive (*Olea europaea*), California blackberry (*Rubus ursinus*), or valley oak (*Quercus lobata*) mechanically inoculated with OLS strains of *X. fastidiosa*. A 500-bp sequence of the 16S-23S ribosomal intergenic region of oleander strains showed 99.2% identity with Pierce's disease strains, 98.4% identity with oak leaf scorch strains, and 98.6% identity with phony peach, plum leaf scald, and almond leaf scorch strains. *Additional keywords*: Graphocephala, Homalodisca coagulata, Homalodisca lacerta, sharpshooter, vector transmission.

Genetics and Resistance
Use of Reciprocal Grafting to Study Brown Stem Rot Resistance in Soybean. M. S. Bachman and C. D. Nickell. Department of Crop Sciences, University of Illinois, Urbana 61801.

Resistance to brown stem rot of soybean has been identified and utilized in cultivar development and germ plasm enhancement. However, little is known about the nature of resistance to this disease. In an attempt to better understand the resistance mechanism by locating the tissue or tissues responsible for resistance, reciprocal grafts were made between brown stem rot-resistant and -susceptible genotypes including near-isogenic lines for resistance gene *Rbs2*. Results of brown stem rot evaluation of grafted plants indicate that brown stem rot resistance is conditioned by the root in all resistance sources evaluated.

Ecology and Population Biology
Primary Disease Gradients of Bacterial Blight of Rice. Christopher C. Mundt, Hafiz U. Ahmed, Maria R. Finckh, Lorna P. Nieva, and Rizal F. Alfonso. Entomology and Plant Pathology Division, International Rice Research Institute, P.O. Box 933, 1099 Manila, Philippines.

The dispersal potential of *Xanthomonas oryzae* pv. *oryzae*, causal agent of bacterial blight of rice (*Oryzae sativa*), was investigated through measurement of primary disease gradients. Plants within individual hills of rice were inoculated, and the number of new lesions in the primary generation of dispersal from these inoculated sources was counted. Two dispersal models that can describe the number of infections at the source (the Kiyosawa and Shiyomi and the modified Gregory) were fit to the lesion counts. Estimated gradient slopes were similar in the 2 years of the study for both gradient models. However, the Kiyosawa and Shiyomi model gave a better fit in both years, as indicated by higher coefficients of determination and significances of slopes and by a more random pattern of residuals. Primary disease gradients were very steep, with half-distances (distances over which lesion numbers are calculated to decrease by half) estimated from the Kiyosawa and Shiyomi model of 0.091 and 0.081 m in 1994 and 1995, respectively. Splash dispersal of *X. oryzae* pv. *oryzae* is the most likely explanation for both the steep slopes measured and the superior fit of the Kiyosawa and Shiyomi model over the modified Gregory model.

Ecology and Population Biology
Assessment of Host-Induced Selection on Three Geographic Isolates of *Heterodera schachtii* Using RAPD and AFLP Markers. M. Kaplan, E. P. Caswell-Chen, and V. M. Williamson. First author: Departments of Plant Pathology and Nematology, University of California, Davis 95616; and second and third authors: Department of Nematology, University of California, Davis.

The hypothesis that host plants exert selection pressure on *Heterodera schachtii* populations was tested. Host selection of genotypes from three genetically distinct isolates of *H. schachtii* was assessed using cabbage, sugar beet, oilseed radish (*Raphanus sativus*), and white mustard (*Sinapis alba*). The plants represent a range of

susceptibility to *H. schachtii* and included *R. sativus* and *S. alba*, because cultivars of those species have been used as trap crops for *H. schachtii* in Europe. Genotypic differences in amplified fragment length polymorphism (AFLP) and random amplified polymorphic DNA (RAPD) markers were detected among the isolates after they reproduced on the different hosts. The poorest host plant, *R. sativus*, resulted in the greatest number of changes in both AFLP and RAPD markers. Oilseed radish selected nematode genotypes in less than four nematode generations. The nematode population genotypes detected by RAPD analyses after selection on oilseed radish were observed even after nematode populations were transferred back to the other three hosts. The genetic markers that were detected after selection were influenced by the genotypes of the original nematode isolates. The results indicate the utility of RAPDs and AFLPs for identifying and monitoring intraspecific genetic variability in nematodes and for understanding nematode population responses to host plants. Nematode management practices such as using resistant cultivars may alter gene frequencies, thereby reducing the efficacy of the tactic and exacerbating the nematode's potential to damage subsequent crops. *Additional keywords*: *Beta vulgaris*, *Brassica oleracea*, cyst nematode, PCR, population genetics.

A Generalized Two-Dimensional Gaussian Model of Disease Foci of Head Blight of Wheat Caused by *Gibberella zeae*. T. C. Paulitz, P. Dutilleul, S. H. Yamasaki, W. G. D. Fernando, and W. L. Seaman. First and second authors: Department of Plant Science; third author: Department of Natural Resource Sciences, Macdonald Campus of McGill University, Ste. Anne de Bellevue, Quebec H9X 3V9 Canada; and fourth and fifth authors: Agriculture and Agri-Food Canada, Plant Research Centre, Ottawa, Ontario K1A 0C6 Canada. Phytopathology 89:74-83. Accepted for publication 1 October 1998. Copyright 1999 The American Phytopathological Society.

A generalized two-dimensional Gaussian model is proposed to describe disease foci of head blight of wheat in plots (100 to 2,500 m^2) originating from small areas (1 to 16 m^2) inoculated with *Gibberella zeae*-colonized corn kernels. These anisotropic, asymmetrical foci arose from ascospores produced in perithecia. The model is $Z = \exp[-(AX^2 + BY^2 + CXY + DX + EY + F)]$, in which Z = the incidence of seed or spikelet infection at point (X,Y) located in the plot, exp = the exponential function, X = the abscissa or spatial coordinate of the point along a given axis (approximately parallel to the average wind vector during the period of spore release in these experiments), Y = the ordinate or spatial coordinate of the point along the axis perpendicular to the X axis (approximately perpendicular to the wind direction in these experiments), A and B = the quadratic coefficients of the second-order polynomial $AX^2 + BY^2 + CXY + DX + EY + F$, C = the bilinear coefficient, D and E = the linear coefficients, and $\exp(-F)$ = the incidence of seed or spikelet infection at the focus peak in which X = 0 and Y = 0. The generalized two-dimensional Gaussian model was tested on data from a circular or isotropic focus, an elliptical or anisotropic focus with two axes of symmetry, and two anisotropic foci with one and zero axis of symmetry. Its goodness-of-fit (r^2 and adjusted r^2) was compared with the inverse power, modified inverse power, exponential, and classical Gaussian models. Submodels using only the linear terms, only the quadratic terms, or combinations selected from stepwise regression procedures using various probabilities to enter and to stay and a procedure maximizing the adjusted r^2 were also considered. Spatial analysis of the residuals was performed using Geary's c coefficient at the first distance class. For the circular and elliptical foci, our model provided a fit similar to the modified inverse power and exponential models. However, for anisotropic foci with one or zero axis of symmetry arising from ascospores influenced by wind direction, the generalized two-dimensional Gaussian model provided a better fit. For these anisotropic foci, the linear term X but not the quadratic term X^2 was generally retained in the model, indicating an exponential gradient in the direction parallel to the wind. In all models, the quadratic term Y^2 was retained, along with Y in some cases, indicating that the gradient in the direction roughly perpendicular to the wind was Gaussian or Gaussian-exponential in shape. The bilinear term XY provided an indication of the orientation of the focus in relation to the axes of the sampling grid. This model has the versatility and parameters (quadratic, bilinear, and linear) to better describe the anisotropy of foci from wind-dispersed spores. *Additional keywords*: disease gradient.

Dynamics of Primary and Secondary Infection in Take-All Epidemics. D. J. Bailey and C. A. Gilligan. Department of Plant Sciences, University of Cambridge, Downing Street, Cambridge, CB2 3EA, England, U.K. Phytopathology 89:84-91. Accepted for publication 4 October 1998. Copyright 1999 The American Phytopathological Society.

Using a combination of experimentation and mathematical modeling, the effects of initial (particulate) inoculum density on the dynamics of disease resulting from primary and secondary infection of wheat by the take-all fungus, *Gaeumannomyces graminis* var. *tritici*, were tested. A relatively high inoculum density generated a disease progress curve that rose monotonically toward an asymptote. Reducing the initial inoculum density resulted in a curve that initially was monotonic, rising to a plateau, but which increased sigmoidally to an asymptotic level of disease thereafter. Changes in the

infectivity of particulate inoculum over time were examined in a separate experiment. Using a model that incorporated terms for primary and secondary infection, inoculum decay, and host growth, we showed that both disease progress curves were consistent with consecutive phases dominated, respectively, by primary and secondary infection. We examined the spread of disease from a low particulate inoculum density on seminal and adventitious root systems separately. Although seminal roots were affected by consecutive phases of primary and secondary infection, adventitious roots were affected only by secondary infection. We showed that the characteristic features of disease progress in controlled experiments were consistent with field data from crops of winter wheat. We concluded that there is an initial phase of primary infection by *G. graminis* var. *tritici* on winter wheat as seminal roots grow through the soil and encounter inoculum, but the rate of primary infection slows progressively as inoculum decays. After the initial phase, there is an acceleration in the rate of secondary infection on both seminal and adventitious roots that is stimulated by the increase in the availability of infected tissue as a source of inoculum and the availability of susceptible tissue for infection.

Biological Control
Biological Control of Fusarium Wilt of Cucumber by Chitinolytic Bacteria.
Pushpinder Paul Singh, Yong Chul Shin, Chang Seuk Park, and Young Ryun Chung. First, second, and fourth authors: Department of Microbiology; and third author: Department of Agricultural Biology, Gyeongsang National University, Chinju 660-701, Korea.
Two chitinolytic bacterial strains, *Paenibacillus* sp. 300 and *Streptomyces* sp. 385, suppressed Fusarium wilt of cucumber (*Cucumis sativus*) caused by *Fusarium oxysporum* f. sp. *cucumerinum* in nonsterile, soilless potting medium. A mixture of the two strains in a ratio of 1:1 or 4:1 gave significantly ($P < 0.05$) better control of the disease than each of the strains used individually or than mixtures in other ratios. Several formulations were tested, and a zeolite-based, chitosan-amended formulation (ZAC) provided the best protection against the disease. Dose-response studies indicated that the threshold dose of 6 g of formulation per kilogram of potting medium was required for significant ($P < 0.001$) suppression of the disease. This dose was optimum for maintaining high rhizosphere population densities of chitinolytic bacteria (log 8.1 to log 9.3 CFU/g dry weight of potting medium), which were required for the control of Fusarium wilt. The ZAC formulation was suppressive when added to pathogen-infested medium 15 days before planting cucumber seeds. The formulation also provided good control when stored for 6 months at room temperature or at 4°C. Chitinase and beta-1,3-glucanase enzymes were produced when the strains were grown in the presence of colloidal chitin as the sole carbon source. Partial purification of the chitinases, followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis and activity staining, revealed the presence of five bands with molecular masses of 65, 62, 59, 55, and 52 kDa in the case of *Paenibacillus* sp. 300; and three bands with molecular masses of 52, 38, and 33 kDa in the case of *Streptomyces* sp. 385. Incubation of cell walls of *F. oxysporum* f. sp. *cucumerinum* with partially purified enzyme fractions led to the release of *N*-acetyl-D-glucosamine (NAGA). NAGA content was considerably greater when pooled enzyme fractions (64 to 67) from *Paenibacillus* sp. were used, because they contained high beta-1,3-glucanase activity in addition to chitinase activity. Suppression of Fusarium wilt of cucumber by a combination of these two bacteria may involve the action of these hydrolytic enzymes.

Ecology and Population Biology
Characterization of Ribosomal DNA from *Venturia inaequalis* and Its Phylogenetic Relationship to rDNA from Other Tree-Fruit *Venturia* Species. G. Schnabel, E. L. Schnabel, and A. L. Jones. Department of Botany and Plant Pathology and the Pesticide Research Center, Michigan State University, East Lansing 48824-1312.
A portion of the 18S ribosomal DNA (rDNA) gene, the internal transcribed spacers (ITS1 and ITS2), and the 5.8S rDNA gene were polymerase chain reaction-amplified from strains and field populations of *Venturia inaequalis* and assessed for genetic variation. A previously reported optional group I intron in the 18S rDNA gene of *V. inaequalis* was detected in 75.0% of 92 strains collected worldwide and in 61.1 and 71.2% of 54 and 59 strains from two Michigan orchards, respectively. Sequence and restriction analysis of rDNA revealed four intron alleles, three of which were present both in worldwide strains and in each field population. Two ITS1 alleles were detected and found to be linked to specific intron alleles. The ITS1-5.8S-ITS2 sequences from *V. asperata*, *V. carpophila*, *V. cerasi*, *V. inaequalis*, *V. nashicola*, *V. pyrina*, and *Cladosporium caryigenum* were compared using phylogenetic analysis. Strains of the *Venturia* species were placed in three distinct monophyletic groups in a phylogenetic tree. The first group comprised *V. inaequalis*; the second, *V. pyrina* and *V. nashicola*; and the third, *V. cerasi*, *V. carpophila*, and *V. asperata*. The described intron and ITS1 alleles in *V. inaequalis* provide genetic markers for subdividing populations of *V. inaequalis*, and the ITS1-5.8S-ITS2 sequences are valuable in determining the

relationship of the species from tree-fruit crops with other *Venturia* species. *Additional keywords*: apple scab, *Carya*, coevolution, *Malus*, *Prunus*, *Pyrus*, Venturiaceae.